Please insert the attached "Sequence Listing" (sheets 1/2 through 2/2), and comprising SEQ ID NOS: 1-6.

Please replace paragraph 0006 with the following:

A1

In yet additional aspect, methods for analyzing gene expression regulation are provided. The methods include obtaining a first set of candidate fragments from the genomic DNA of a first sample, where the first sample is a control sample; obtaining a second set candidate fragments from the genomic DNA of a second sample, wherein the second sample is treated; and comparing the first and second sets of candidate fragments. The candidate fragments can be obtained using DNA foot printing technology. The second sample may be treated with a pharmaceutical agent or with an environmental change. The step of comparing candidate fragments may include hybridizing the first and second sets of candidate fragments with the same collection of nucleic acid probes. In some other embodiments, the step of comparing candidate fragments may include hybridizing the first and second sets of candidate fragments with a first and second collections of nucleic acid probes. The first and second collection of nucleic acid probes can be the same. The nucleic acid probes may be immobilized on a collection of beads or optical fibers or on a substrate. Preferably, the collection of nucleic acid probes contains at least 10,000, 50,000, 100,000, or 1,000,000 probes. The nucleic acid probes may be oligonucleotide probes, preferably between 10-50 in length. In some embodiments, the probes tile genomic sequences of interest. In preferred embodiments, at least one of the binding proteins is unknown.

Please replace paragraph 0007 with the following:

A2

The accompanying drawings, which are incorporated in and form a part of this specification, illustrate embodiments of the invention and, together with the description, serve to explain the principles of the invention: